



## Pretreatment of the yeast antagonist, *Candida oleophila*, with glycine betaine increases oxidative stress tolerance in the microenvironment of apple wounds

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### ABSTRACT

In response to wounding, harvested fruit tissues of apple and citrus exhibit the production of reactive oxygen species (ROS). ROS production is greater when yeast antagonists used as biocontrol agents are applied in the wounds. These phenomena result in an oxidative stress environment for the yeast antagonists. It has been demonstrated that pre-exposure of some of these yeast antagonists to sublethal abiotic stress (heat or hydrogen peroxide), or stress-ameliorating compounds such as glycine betaine (GB) can induce subsequent oxidative stress tolerance in the antagonistic yeast. The increased level of oxidative stress tolerance has been demonstrated *in vitro* and is characterized by higher levels of antioxidant gene expression, increased production of trehalose, and lower levels of ROS when yeast are exposed to a subsequent oxidative stress. The current study determined whether or not the effects of GB on yeast antagonists determined *in vitro* persist and are present *in planta* when yeast are applied to wounded apples. The effect of exogenous GB on the production of ROS in the yeast antagonist, *Candida oleophila*, was determined after the yeast was placed in apple wounds. Oxidative damage to yeast cells recovered from apple wounds was also monitored. Results indicated that GB treatment improved the adaptation of *C. oleophila* to apple fruit wounds. Compared to untreated control yeast cells, GB-treated cells recovered from the oxidative stress environment of apple wounds exhibited less accumulation of ROS and lower levels of oxidative damage to cellular proteins and lipids. Additionally, GB-treated yeast exhibited greater biocontrol activity against *Penicillium expansum* and *Botrytis cinerea*, and faster growth in wounds of apple fruits compared to untreated yeast. The expression of major antioxidant genes, including *peroxisomal catalase*, *peroxiredoxin TSA1*, and *glutathione peroxidase* was elevated in the yeast by GB treatment. This study supports the premise that activation of antioxidant response in biocontrol yeast can improve biocontrol efficacy.

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### 1. Introduction

The use of biocontrol agents to manage postharvest diseases of fruits has shown great potential in recent years (Droby et al., 2011; Jamalizadeh et al., 2011; Sharma et al., 2009; Spadaro and Gullino, 2004). Among these agents, the utilization of yeasts has been emphasized (Janisiewicz et al., 2010; Wisniewski et al., 2007). The yeast antagonist, *Candida oleophila*, has demonstrated biocontrol efficacy against postharvest diseases of various fruits, including apple (Mercier and Wilson, 1995), peach (Droby et al., 2003), pear (Lahlali et al., 2011), grapefruit (Droby et al., 2002) and strawberry (Lima et al., 1997).

The ability to survive and proliferate in host tissues is crucial for the efficacy of antagonistic yeasts (Droby et al., 2009; Janisiewicz and Korsten, 2002). When applied to fruit surfaces and wounds, biocontrol

agents encounter an oxidative stress environment that may affect their viability and efficacy (Castoria et al., 2003; Macarasin et al., 2010). The production of reactive oxygen species (ROS) in fruit tissue could in turn induce ROS accumulation in yeast cells, and result in oxidative damage thus compromising cell function (Garre et al., 2010; Saharan and Sharma, 2010). Macarasin et al. (2010) reported that *C. oleophila* and another biocontrol yeast, *Metschnikowia fructicola*, generated high levels of ROS when applied to intact or wounded apple fruits. HersHKovitz et al. (2012) reported that high amounts of ROS were detected in *M. fructicola* cells recovered from wounded grapefruit tissue. Therefore, enhancing tolerance to oxidative stress in fruit tissue may represent a useful strategy for improving the effectiveness of antagonistic yeasts.

As a major compatible solute, glycine betaine (GB, N, N, N-trimethyl glycine) plays a vital role in osmotic adjustment in various organisms, including bacteria, fungi, and plants (de Zwart et al., 2003; Rhodes and Hanson, 1993). GB has also been reported to have a protective function by inducing antioxidant compounds under stress conditions. For example, exogenous application of GB enhanced antioxidant scavenging compounds in tobacco (Banu et al., 2009), wheat (Raza et al.,

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2007), rice (Farooq et al., 2008) and maize (Nawaz and Ashraf, 2010). In microorganisms, GB application has been shown to be an effective osmoprotectant in *Escherichia coli* (Cayley and Record, 2003), *Pichia pastoris* (Wang et al., 2007) and *Penicillium fellutanum* (Park and Gander, 1998). More recently, accumulation of GB and ectoine in osmotic stress adaptation of biocontrol bacteria, *Bacillus amyloliquefaciens* and *Microbacterium oleovorans*, increased the potential for biocontrol of *Fusarium verticillioides* in maize (Sartori et al., 2012). GB was shown to improve H<sub>2</sub>O<sub>2</sub>-induced oxidative stress tolerance by elicitation of antioxidant enzyme activity in the biocontrol yeast, *Cystofilobasidium infirmominatum* (Liu et al., 2011b). However, there is little information about the effect of GB on the antioxidant response of biocontrol yeast in the actual microenvironment of fruit wounds. The objective of the present study was to determine the effect of GB on the antioxidant response and biocontrol efficacy of *C. oleophila* after they were applied to apple wounds. More specifically, this study investigated the effect of a pretreatment of *C. oleophila* with GB on (i) subsequent ROS accumulation, protein carbonylation and lipid peroxidation in yeast recovered from apple wounds (ii) the induction of antioxidant genes, including *peroxisomal catalase* (CAT), *peroxiredoxin TSA1* (TSA1) and *glutathione peroxidase* (GPX) in *C. oleophila*, again in yeast recovered from apple wounds, and (iii) yeast viability in apple fruit wounds and biocontrol efficacy against *Penicillium expansum* and *Botrytis cinerea*.

## 2. Materials and methods

### 2.1. Yeast

*C. oleophila* (strain I-182) was isolated from the surface of tomato fruit as documented in a previous study (Wilson et al., 1993), and grown in a yeast peptone dextrose (YPD) broth (10 g of yeast extract, 20 g of peptone and 20 g of dextrose in 1000 ml of water). Twenty milliliters of YPD (Fisher Scientific, Fair Lawn, NJ, USA) was placed in 50-ml conical flasks and inoculated with *C. oleophila* at an initial concentration of 10<sup>5</sup> cells/ml determined with an automated cell counter, Cellometer Vision (Nexcelom Bioscience, Lawrence, MA, USA). Yeast cultures were incubated at 25 °C at 200 rpm on a rotary shaker (New Brunswick Scientific, Edison, NJ, USA).

### 2.2. Pathogens

*P. expansum* and *B. cinerea* were isolated from infected apple fruits and maintained on potato dextrose agar (PDA) (Difco, Sparks, MD, USA) at 4 °C (Liu et al., 2012). In order to reactivate the culture and verify their ability to cause disease, the pathogens were inoculated into wounds of apple fruit and re-isolated onto PDA once the infection was established. Spore suspensions of the two pathogens were obtained from 2-week-old cultures on PDA at 25 °C. The spore number was calculated with a Cellometer Vision, and the concentration was adjusted to 1 × 10<sup>5</sup> spores/ml with sterile distilled water.

### 2.3. Fruits

Apples (*Malus x domestica* Borkh. cv. Granny Smith) were harvested at commercial maturity. Fruits without wounds or rot were selected based on uniformity of size, disinfected with 2% (v/v) sodium hypochlorite for 2 min, rinsed with tap water and air dried (Li et al., 2008). These fruits were used in a subsequent biocontrol assay.

### 2.4. GB treatment of *C. oleophila*

Overnight yeast cultures were pelleted at 8000 g for 3 min and washed three times with sterile distilled water in order to remove residual medium, according to Li and Tian (2006). Washed cells were resuspended in the same volume (20 ml) of fresh YPD, supplemented

with GB at the final concentration of 1 mM and incubated at 25 °C for 2 h at 200 rpm. The chosen concentration was based on previous studies (Boncompagni et al., 1999; Liu et al., 2011b) and a preliminary experiment. Control cells were subjected to the same process but without GB treatment. Cells were harvested by centrifugation at 8000 g for 3 min and washed three times with sterile distilled water in order to remove any residual GB and medium. The GB-treated (GB) and non-GB-treated (NGB) yeast samples were suspended in water at 5 × 10<sup>7</sup> cells/ml for the following experiments.

### 2.5. Determination of intracellular ROS accumulation in *C. oleophila* in response to apple fruit tissue

Three wounds (4 mm deep × 3 mm wide) were made on the equator of each fruit with a sterile nail. A 10 µl suspension of GB or NGB *C. oleophila* cells (5 × 10<sup>7</sup> cells/ml) was applied to each wound and allowed to air dry. Treated fruits were placed in a covered plastic food tray, and each tray was enclosed in a polyethylene bag and stored at 25 °C. Wound sites were removed using a 9 mm cork borer under aseptic condition after 6, 12, 24 and 48 h. The time point before inoculation into wounds served as time 0. Yeast cells were washed from 20 cylinders (4 mm deep) obtained from wounds of 10 fruits and cut into quarters, with 20 ml phosphate buffered saline (PBS, pH 7.0) in 50-ml conical flasks shaken at 200 rpm for 30 min on rotary shaker (Hershkovitz et al., 2012). Then yeast cells were pelleted at 8,000 g for 3 min and resuspended at the concentration of 1 × 10<sup>7</sup> cells/ml in 500 µl PBS containing 25 µM carboxy-H2DCFDA (Invitrogen, Eugene, OR, USA), and the suspensions were incubated in the dark at 30 °C for 1 h (Liu et al., 2011a, b). The yeast cells were then washed twice with PBS buffer and resuspended in 96-well plate (200 µl PBS per well). The fluorescence intensity was measured at an excitation of 485 nm and emission of 530 nm using a fluorescence microplate reader (Synergy™ HT, BioTek Instruments, Winooski, VT, USA). The values of NGB and GB cells at different time points were calculated as the relative fluorescence intensity, compared to NGB cells at time 0 (Dirmeier et al., 2002; Oh and Lim, 2008). There were three replicates in each treatment, and the experiment was repeated three times.

### 2.6. Determination of protein carbonylation and lipid peroxidation in *C. oleophila*

Yeast samples (GB or NGB) were collected from fruit wounds at 0, 6, 12, 24 and 48 h using the same method as described above. Yeast cells were disrupted in liquid nitrogen with the aid of a mortar and pestle. Protein carbonylation was measured as an indicator of oxidative damage to proteins (Liu et al., 2011b). Proteins were extracted from the samples using 500 µl of 50 mM KH<sub>2</sub>PO<sub>4</sub> buffer (pH 7.5) containing 10 mM Tris, 2 mM MgCl<sub>2</sub>, 2 mM EGTA and 1 mM PMSF. Aliquots of extract were reacted with 500 µl of 10 mM 2,4-dinitrophenylhydrazine (DNPH) dissolved in 2.5 M HCl or 2.5 M HCl without DNPH (blank control) in the dark at room temperature with vortex every 15 min for 1 h. Proteins were precipitated with 20% trichloroacetic acid (TCA, w/v) and kept on ice for 10 min. After centrifuging at 3000 g for 20 min, protein pellets were washed with ethanol-ethyl acetate (1:1, v/v) and dissolved in 6 M guanidine hydrochloride with 20 mM KH<sub>2</sub>PO<sub>4</sub> (pH 2.3). The absorbance was recorded at 380 nm after centrifugation at 9500 g for 10 min. The carbonyl content was calculated using the molar absorption coefficient of 22,000/M/cm, and expressed as nmol per mg protein.

To assay lipid peroxidation, a method based on the reaction of thiobarbituric acid with malondialdehyde (MDA) was used. Detection of thiobarbituric acid-reactive species (TBARS) was carried out as described by Garre et al. (2010). Disrupted yeast samples were resuspended in 500 µl of 50 mM KH<sub>2</sub>PO<sub>4</sub> buffer (pH 6.0) containing 10% (w/v) trichloroacetic acid, and centrifuged at 3,000 g for 10 min.

Supernatants were mixed with 100  $\mu$ l of 0.1 M EDTA and 600  $\mu$ l of 1% (w/v) thiobarbituric acid. After cooling down, the absorbance was measured at 532 nm. The MDA content was calculated using the molar absorption coefficient of 153,000/M/cm, and expressed as nmol per mg protein.

Protein content was measured using the Bradford assay (Bradford, 1976). Bovine serum albumin (Sigma-Aldrich, St. Louis, MO, USA) was used as a standard. There were three replicates in each treatment, and the experiment was repeated three times.

## 2.7. RNA isolation and semi-quantitative RT-PCR analysis of antioxidant gene expression

Total RNA from yeast samples (NGB or GB) collected from fruit wounds at 0, 6, 12, 24 and 48 h was isolated using an RNeasy Mini Kit (Qiagen Science, Germantown, MD, USA) according to the manufacturer's instructions (Liu et al., 2011a). Extracted RNA was treated with TURBO™ DNase (Ambion, Austin, TX, USA) and purified again with RNeasy. Aliquots of 1  $\mu$ g total RNA were used for first strand cDNA synthesis in 20  $\mu$ l reaction volume with 100 units of M-MLV reverse transcriptase (Ambion, Austin, TX, USA). Transcript levels of 18S rRNA gene served as an internal control (Lee et al., 2008; Pacheco et al., 2009). Cycling parameters for each gene amplification were 95 °C for 5 min; 25 cycles of 95 °C for 30 s, specific annealing temperature for 30 s, and 72 °C for 30 s; and finally 72 °C for 10 min. The primer pairs and annealing temperatures of the antioxidant genes *CAT*, *TSA1* and *GPX* were designed according to Liu et al. (2012). PCR products were cloned and sequenced to verify the identity. Quantification of transcript expression level was based on the band intensity on an ethidium-bromide-stained gel using Scion Image Software (Scion Corp., Frederick, Maryland, USA) according to Oliveira et al. (2010). There were three replicates in each treatment, and the experiment was repeated three times.

## 2.8. Population dynamics of *C. oleophila* in wounds of apple fruits

Three wounds (4 mm deep  $\times$  3 mm wide) were made on the equator of each fruit with a sterile nail. A 10  $\mu$ l suspension of GB or NGB cells of *C. oleophila* ( $5 \times 10^7$  cells/ml) was applied to each wound. Fruit samples were then collected at 6, 12, 24 and 48 h after treatment and yeast populations were determined as described by Cao et al. (2010). Briefly, yeasts were recovered by removing 20 samples of wounded tissues of 10 fruits with a 9 mm cork borer. Samples were then ground with a mortar and pestle in 20 ml sterile distilled water. Then, 50  $\mu$ l of serial 10-fold dilutions were spread on YPD agar plates. Samples taken at 1 h after treatment served as time 0. Colonies were counted after incubation at 25 °C for 3 days and expressed as the Log<sub>10</sub> CFU per wound. There were three replicates in each treatment, and the experiment was repeated three times.

## 2.9. Biocontrol assay of *C. oleophila* against postharvest diseases of apple fruits

Biocontrol efficacy was tested according to a previous study (Liu et al., 2009). Three wounds (4 mm deep  $\times$  3 mm wide) were made on the equator of each fruit with a sterile nail. A 10  $\mu$ l suspension of non-GB-treated (NGB) or GB-treated (GB) cells of *C. oleophila* ( $5 \times 10^7$  cells/ml) was applied to each wound. Sterile distilled water served as a control. When fruits were air-dried, 10  $\mu$ l of either *P. expansum* or *B. cinerea* suspension ( $1 \times 10^5$  spores/ml) were inoculated into each wound. Treated fruits were placed in a covered plastic food tray. Each tray was enclosed with a polyethylene bag in order to maintain high humidity (about 95% relative humidity) and stored at 25 °C. Disease incidence and lesion diameter of apple fruits were recorded after 4 days. Each treatment contained three replicates with ten fruits per replicate and the experiment was repeated three times.

## 2.10. Data analysis

All statistical analyses were performed with SPSS version 13.0 (SPSS Inc., Chicago, IL, USA). Two-way analysis of variance (ANOVA) analysis was performed on data where treatment and time were variables, and mean separation was determined for non-GB-treated control (NGB) and GB-treated (GB) yeast samples at each time point using a Student's *t*-test. Data with a single variable (treatment) in biocontrol test were analyzed by one-way ANOVA, and mean separations were performed by Duncan's multiple range tests. Differences at  $P < 0.05$  were considered significant. Data presented in this paper were pooled across three independent repeated experiments, as the interaction between treatment and experiment variables was not significant.

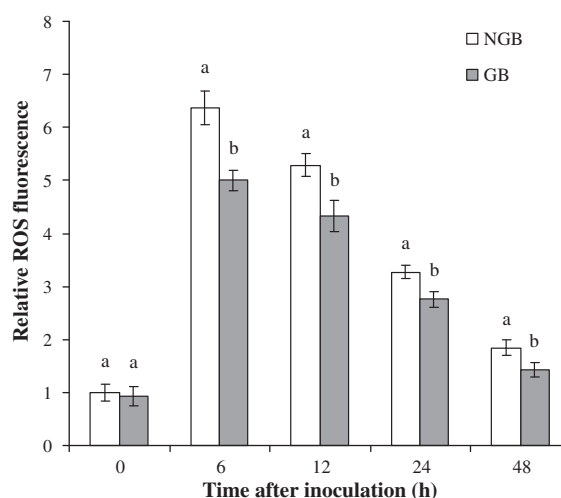
## 3. Results

### 3.1. ROS accumulation of *C. oleophila*

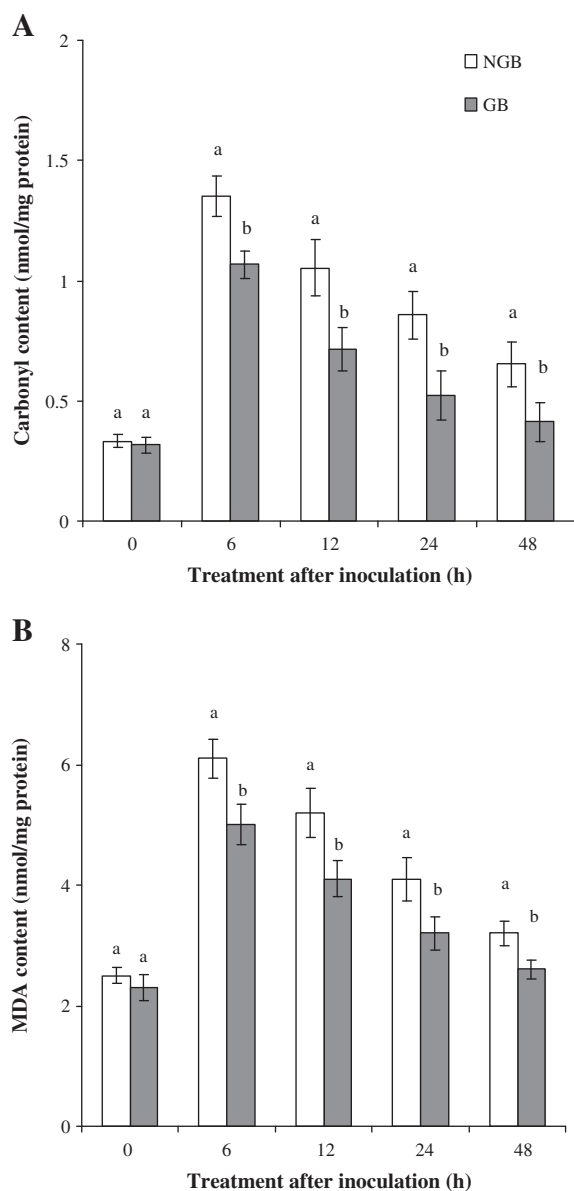
At time 0, prior to inoculation into apple wounds, ROS levels in both GB and NGB cells were at a low level (Fig. 1). ROS accumulation peaked in yeast cells recovered from apple wounds at 6 h after inoculation and gradually decreased over the 48 h period in which samples were taken. Even at 48 h, ROS levels were still above those observed at 0 h. Both treatment and duration of time in the wounds had a significant ( $P < 0.05$ , two-way ANOVA analysis) effect on intracellular ROS accumulation in *C. oleophila*. GB-treated cells exhibited a significantly ( $P < 0.05$ , Student's *t*-test) lower ROS level compared to NGB cells at all of the four time points (after time 0) in fruit wounds. After 48 h at fruit wounds, the relative value of ROS level in GB cells was 1.43 while that of NGB cells was 1.84.

### 3.2. Protein carbonylation and lipid peroxidation

To investigate the protective effect of GB against oxidative damage to proteins and lipids, carbonyl content (indicator of protein oxidation) and MDA content (indicator of lipid peroxidation) in *C. oleophila* cells recovered from wounds were measured (Fig. 2). The pattern in the levels of both carbonyl and MDA content were similar to what was observed for ROS accumulation. Levels of MDA were higher than carbonyl content, although both parameters increased by approximately three-



**Fig. 1.** ROS accumulation in non-glycine betaine-treated (NGB) and glycine betaine-treated (GB) cells of *C. oleophila* recovered from apple wounds at varying periods of time following inoculation. The relative ROS fluorescence values of NGB and GB cells at different time points were calculated as the relative fluorescence intensity compared to NGB cells at time 0. Data presented are the means  $\pm$  sd of three independent experiments where each experiment consisted of three biological replicates for a total of  $n = 9$ . Columns with different letters at each time point indicate significant differences according to Student's *t*-test ( $P < 0.05$ ).

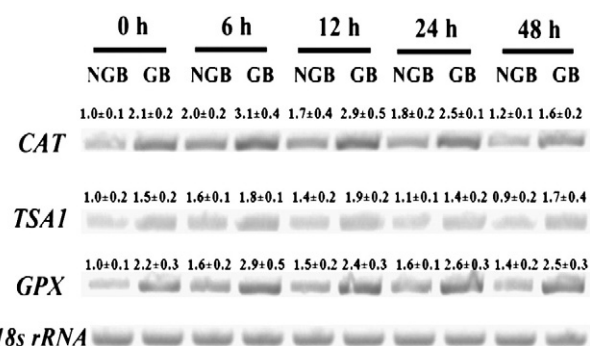


**Fig. 2.** Protein carbonylation (A) and lipid peroxidation (B) in non-glycine betaine-treated (NGB) and glycine betaine-treated (GB) cells of *C. oleophila* recovered from apple wounds at varying periods of time following inoculation. Data presented are the means  $\pm$  sd of nine pooled replicates. Columns with different letters at each time point indicate significant differences according to Student's *t*-test ( $P < 0.05$ ).

fold at their maximum. At time 0, prior to inoculation into apple wounds, carbonyl and MDA contents in NGB and GB cells were low and not significantly different in GB and NGB cells. Inoculation of yeast into apple wounds resulted in a marked increase in both carbonyl and MDA content during the first 12 hours. While elevated in both, GB cells had a significantly ( $P < 0.05$ , Student's *t*-test) lower carbonyl content and MDA content than NGB cells at all of the four time points after time 0.

### 3.3. Antioxidant gene expression

Sequencing results confirmed that the PCR product obtained from each pair of primers was 100% identical to each target gene (data not shown). Semi-quantitative analysis of gene expression of yeast samples at time 0 (the time point after 2-h GB treatment but prior to inoculation into fruit wounds) indicated that GB treatment induced the expression of *CAT*, *TSA1* and *GPX* in *C. oleophila* cells (Fig. 3). The inductive effect was

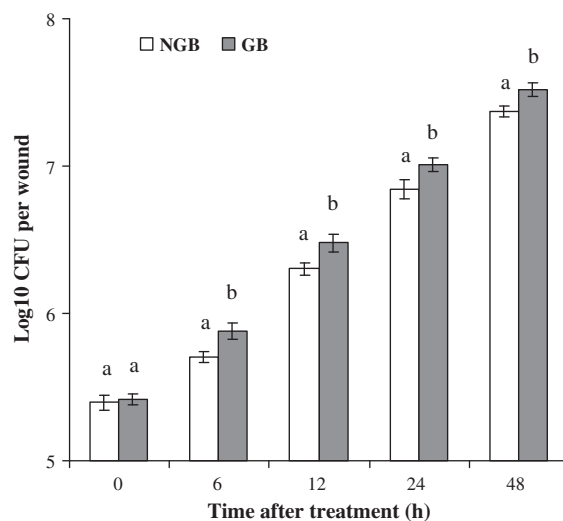


**Fig. 3.** Expression of some antioxidant genes (*CAT*, *TSA1* and *GPX*) in non-glycine betaine-treated (NGB) and glycine betaine-treated (GB) cells of *C. oleophila* recovered from apple wounds at varying periods of time following inoculation. The 18S rRNA gene was used as a control for normalizing mRNA quantity. The mean level of gene expression, as determined by densitometry, relative to the sample at Time 0 is shown above each band ( $n = 9 \pm$  sd). GB cells had significantly higher levels of expression compared to NGB cells for all three genes at all the time periods evaluated ( $P < 0.05$ , Student's *t*-test).

more apparent for *CAT* and *GPX* than with *TSA1*. Moreover, the inductive effect of GB treatment on *C. oleophila* was evident at least 2 d after inoculation into apple wounds (Fig. 3). Statistical analysis indicated that GB yeast cells had higher levels of expression compared to NGB cells for all three genes at all time periods measured ( $P < 0.05$ , Student's *t*-test).

### 3.4. Population dynamics of *C. oleophila* in apple wounds

Regardless of whether or not the yeast cells had been pre-treated with GB, *C. oleophila* multiplied quickly in apple fruit wounds (Fig. 4). The GB treatment, however, did have a significant impact on yeast growth in apple wounds ( $P < 0.05$ , two-way ANOVA analysis). After 12 h, the number of the GB and NGB yeast increased nearly ten-fold. The population of GB-treated cells, however, was significantly ( $P < 0.05$ , Student's *t*-test) higher than the population of NGB-treated cells at all the time points after time 0.



**Fig. 4.** Population dynamics of *C. oleophila* in wounds of apple fruits stored at 25 °C. Fruits were wounded and inoculated with 10  $\mu$ l of non-glycine betaine-treated (NGB) or glycine betaine-treated (GB) cell suspension of *C. oleophila* at  $5 \times 10^7$  cells/ml. Yeast were recovered from wounds at varying periods of time following inoculation and colonies were counted after incubation at 25 °C for 3 days and expressed as the Log<sub>10</sub> CFU per wound. Data presented are the means  $\pm$  sd of nine pooled replicates. Columns with different letters at each time point indicate significant differences according to Student's *t*-test ( $P < 0.05$ ).



### 3.5. Biocontrol efficacy of *C. oleophila*

As shown in Fig. 5, *C. oleophila* significantly reduced both disease incidence and lesion diameter of both blue mold and grey mold of apple caused by *P. expansum* and *B. cinerea*, respectively. Importantly, GB yeast exhibited a greater level of efficacy than NGB yeast for both disease incidence and lesion diameter ( $P < 0.05$ , one-way ANOVA).

## 4. Discussion

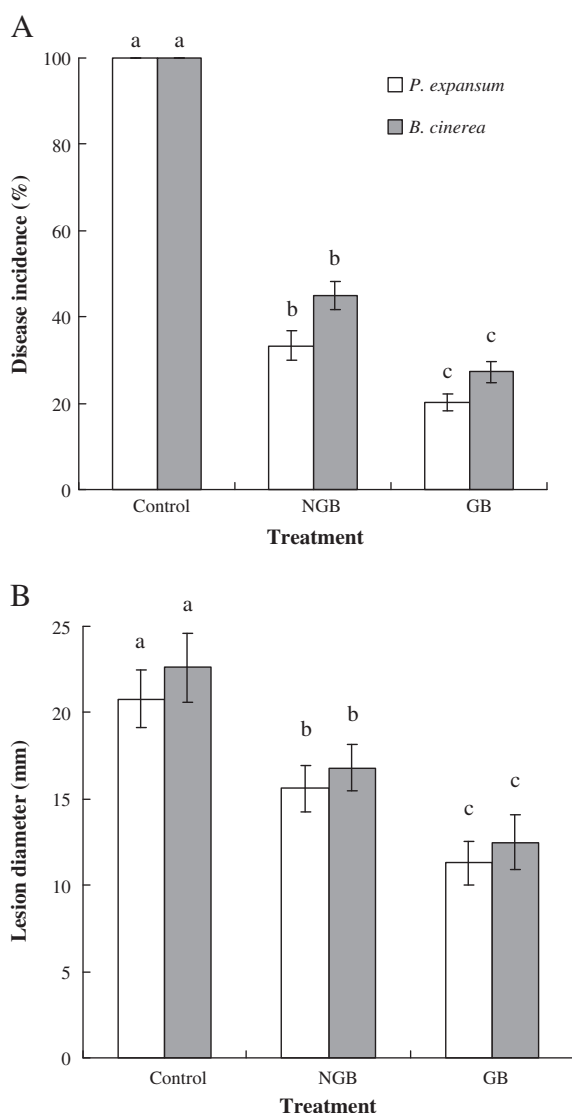
The oxidative environment plays an important role in biocontrol systems involving a biocontrol agent, pathogen, and host (Hershkovitz et al., 2012; Macarasin et al., 2007, 2010). Cells of fruit tissue bordering the edge of wounds undergo an oxidative burst producing high levels of hydrogen peroxide (Macarasin et al., 2007) while yeast antagonists placed on the surface or within wounds of fruit also exhibit a large increase in ROS (Macarasin et al., 2010). The application of yeast to

wounded fruit tissue will also stimulate host ROS production over and above the level induced by wounding alone (Macarasin et al., 2010). Thus there is considerable interaction between the biocontrol agent and host in determining the redox environment at the very site where the biocontrol agent is expected to inhibit and control a specific pathogen. Additionally, the redox environment can either stimulate or be detrimental to different fungal pathogens (Lee and Bostock, 2007; Williams et al., 2011). Regardless of the source of ROS production, it appears that yeast antagonists used to control postharvest diseases of fruits are exposed to oxidative stress (Macarasin et al., 2010; Tolaini et al., 2010). Because of this, Castoria et al. (2003) indicated that microbial antagonists with a high level of oxidative stress tolerance have greater potential as postharvest biocontrol agents. Alternatively, improving the oxidative stress tolerance of biocontrol agents during the formulation process (Liu et al., 2009) or pretreatment of the antagonist prior to application with either a sublethal stress or stress-ameliorating compound (Liu et al., 2011a & b) may also represent a useful strategy for increasing the performance of postharvest biocontrol yeasts.

The main objective of the present study was to determine if the oxidative stress tolerance induced in yeast *in vitro* by pretreatment with a stress-ameliorating compound (glycine betaine) would persist in yeast after they were applied and subsequently recovered from wounded fruit tissues. In a previous *in vitro* study, utilizing the antagonist *C. infirmominiatum*, glycine betaine was shown to be effective in reducing ROS accumulation (Liu et al., 2011b). In the current study, the beneficial effect of glycine betaine in improving oxidative stress tolerance was demonstrated in *C. oleophila* after they were inoculated and recovered from apple wounds (Fig. 1). The results from both studies support the premise that oxidative stress tolerance in antagonistic yeast can be increased by exposure to exogenous GB and that the increased level of tolerance is associated with the enhancement of biocontrol efficacy. Exogenous GB has been reported to modulate antioxidant enzymes and improve stress tolerance in plants (Farooq et al., 2008; Nawaz and Ashraf, 2010; Raza et al., 2007), animal cells (Alfieri et al., 2002; Monobe et al., 2006), and human cells (Craig, 2004). Additionally, intracellular accumulation of GB was shown to be associated with improved osmotic and thermal stress tolerance in the bacterium, *Pantoea agglomerans*, which is used as a postharvest biocontrol agent (Cañamás et al., 2007; Teixidó et al., 2005).

High levels of ROS, in the absence of an effective scavenging system, can cause oxidative damage to cell components including proteins, lipids and nucleic acids, resulting in compromised cell function (Branduardi et al., 2007; Reverter-Branchat et al., 2004). The level of carbonyl groups present and MDA content are widely used as indicators of oxidative damage to proteins and lipids, respectively (Abegg et al., 2010; Li et al., 2010). The data in Fig. 2 indicated that lower carbonyl and MDA levels were detected in GB cells compared to NGB cells recovered from apple wounds. These findings are consistent with our previous finding that GB treatment significantly reduced protein carbonylation and lipid peroxidation in *C. infirmominiatum* *in vitro* when the yeast was exposed to oxidative stress (Liu et al., 2011b). Banu et al. (2009) also found that GB treatment reduced ROS accumulation and lipid peroxidation in tobacco cells under salt stress. The reduced oxidative damage to yeast cells may be due to the function of glycine betaine reported by Einset and Connolly (2009). They suggested that GB blocks ROS signaling by activating antioxidant genes thus reducing the accumulation of ROS.

The enzymatic detoxification of ROS is dependent on the upregulation of antioxidant genes such as CAT, TSA1 and GPX (Collinson et al., 2002; Nakagawa et al., 2010; Wu et al., 2007). Our data indicate that GB treatment upregulated the expression of these three genes in *C. oleophila* cells and that elevated expression of these genes persisted after the yeast were inoculated into apple wounds (Fig. 3). Similar results have been reported by Banu et al. (2009), who reported that GB enhanced the gene expression of CAT and lignin-forming peroxidase in tobacco cells under salt stress. Therefore, the induction of antioxidant



**Fig. 5.** Biocontrol efficacy of *C. oleophila* against *P. expansum* and *B. cinerea* on apple fruits stored at 25 °C. Fruits were wounded and inoculated with 10 µl of sterile water (control), or either a non-glycine betaine-treated (NGB) or glycine betaine-treated (GB) cell suspension of *C. oleophila* at  $5 \times 10^7$  cells/ml. Fruits were air-dried and then wounds were inoculated with either 10 µl of *P. expansum* or *B. cinerea* at  $1 \times 10^5$  spores/ml. Disease incidence (A) and lesion diameter (B) in apple fruits were recorded after 4 days. Data presented are the means  $\pm$  sd of nine pooled replicates. Columns with different letters indicate significant differences according to Duncan's multiple range test ( $P < 0.05$ ).

gene expression in *C. oleophila* by exogenous GB may be a key factor in lowering ROS levels and ameliorating oxidative damage, thus improving the viability of yeast cells in fruit wounds.

Cell viability has a direct influence on the population dynamics of biocontrol agents in fruit wounds and high population density is considered an advantage in competing for nutrients and space, both of which play a major role in biocontrol efficacy (Droby et al., 2009; Wisniewski et al., 2007). It is notable that the population of GB-treated cells of *C. oleophila* grew more rapidly than NGB-treated cells in wounds of apple fruits during the 48 h time period sampled (Fig. 4). This observation is in agreement our previous report on the stimulating effect of GB on growth of another yeast species, *C. infirmominiatum* (Liu et al., 2011b), as well as the reported effect on bacteria (Boniole et al., 2009; Delamare et al., 2003). The first 48 hours after inoculation in apple wounds is crucial for pathogen germination and infection (Li et al., 2008). Thus, the higher population of GB-treated yeast cells in this time period, compared to NGB-treated cells (Fig. 5), may also have contributed to the improved performance in biocontrol of both *B. cinerea* and *P. expansum*.

In conclusion, we found that a pretreatment of the yeast, *C. oleophila*, with glycine betaine could reduce intracellular ROS accumulation, as well as protein and lipid oxidation even after the yeast were applied and then recovered from apple wounds. The increased level of oxidative stress tolerance persisted for at least 48 h following wound inoculation. The reduction in ROS accumulation and oxidative damage resulting from the GB treatment was associated with the upregulation of several antioxidant genes.

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